STIC Biotechnology Systems Branch

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Application Serial Number: _10/527,571_
Source: _PCT_
Date Processed by STIC: _01/31/2006_

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Revised 01/24/05

PCT

RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: US/10/527,571   TIME: 15:59:57

        Input Set : **N:\SMITH\PTO.TS.txt**
        Output Set: **N:\CRF4\01312006\J527571.raw**

   3 <110> APPLICANT: Syngenta Participations AG
   4   Stam, Lynn
   5   Kamdar, Kim
   6   Spana, Eric
   7   Bachmann, Jane
   9 <120> TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that
  10   Encode Proteins Essential for Viability and Uses Thereof
  12 <130> FILE REFERENCE: 70131WOPCT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/527,571
C--> 15 <141> CURRENT FILING DATE: 2005-03-14
  17 <150> PRIOR APPLICATION NUMBER: 60/422,377
  18 <151> PRIOR FILING DATE: 2002-10-29
  20 <160> NUMBER OF SEQ ID NOS: 381
  22 <170> SOFTWARE: PatentIn version 3.1

*Does Not Comply
Corrected Diskette Needed*

CP9-4,5,6)

ERRORED SEQUENCES

7736 <210> SEQ ID NO: 61
7737 <211> LENGTH: 1022
7738 <212> TYPE: PRT
7739 <213> ORGANISM: Drosophila melanogaster
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7748   20   25   30
7751 Asp Ala Lys Gly Gly Lys Ser Gly Lys Val Gly Asn Val Glu Arg Lys
7752   35   40   45
7755 Leu Thr Ala Leu Asn Gln Leu Asp Ala Tyr Val Gly Asn Leu Pro Ala
7756   50   55   60
7759 Gly Ala Leu Val Leu Pro Thr Gly Thr Pro Val Ala Ser Thr Gly Ala
7760 65   70   75   80
7763 Pro Ser Thr Gly Val Ile Gly Asn Pro Pro Ala Ala Ala Thr Gly Ala
7764   85   90   95
7767 Pro Pro Met Thr Ala Ala Asn Ser Arg Glu Leu Leu Glu Leu Leu Val
7768   100   105   110
7771 Lys Ile Thr Asp Glu Ile Ser Tyr Glu Asp Val Glu Met Gly Glu Leu
7772   115   120   125
7775 Lys Glu Val Ala Ser Lys Ile Phe Gln Leu Tyr Gln Leu Gln Glu Arg
7776   130   135   140
7779 Asp Ser Asp Thr Ser Ile Arg Val Lys Leu Leu Glu Leu Leu Ser Gly
7780 145   150   155   160

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Input Set : N:\SMITH\PTO.TS.txt
Output Set: N:\CRF4\01312006\J527571.raw

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7783 Leu Gly Cys Glu Cys Ala Thr Glu Gln Ala Leu Thr Met Ile Ile Asp
7784             165             170             175
7787 Tyr Phe Ile Phe Leu Leu Arg Lys Glu Val Ser Gln Lys Val Leu Ala
7788             180             185             190
7791 Gln Gly Met Met Cys Leu Phe Arg Ile Gly Glu Arg Arg Lys His Met
7792         195             200             205
7795 Leu Pro Ile Ser Tyr Lys Thr Gln Val Ala His Leu Ala Lys Glu Gln
7796     210             215             220
7799 Leu Arg Ser Gly Ser Ala His Thr Gln Lys Asn Ala Met Leu Val Ile
7800 225             230             235             240
7803 Gly Arg Phe Ala Thr Lys Met Glu Gly Glu Arg His Tyr Val Trp Lys
7804             245             250             255
7807 Leu Ala Phe Tyr Ile Asp Ser Gln Asp Ser Ser Val Arg Ala Gln Ala
7808             260             265             270
7811 Leu His Ala Leu Leu Thr Leu Gly Glu Arg Gly Ser Gln Leu Pro Ala
7812         275             280             285
7815 Val Leu Tyr Lys Arg Ala Val Glu Ala Met Lys Asp Asp Tyr Glu Cys
7816     290             295             300
7819 Val Arg Lys Glu Ala Leu Gln Leu Val Phe Met Leu Gly Asn Arg His
7820 305             310             315             320
7823 Pro Asp Tyr Ile Leu Pro Ser Asp Arg Gln Gln Glu Glu Leu Arg Met
7824             325             330             335
7827 Ile Asp Ala Ala Phe Ser Lys Val Cys Glu Ala Leu Cys Asp Leu Ser
7828             340             345             350
7831 Leu Gln Ile Arg Val Leu Ala Ala Glu Leu Leu Gly Gly Met Thr Ala
7832         355             360             365
7835 Val Ser Arg Glu Phe Leu His Gln Thr Leu Asp Lys Lys Leu Met Ser
7836     370             375             380
7839 Asn Leu Arg Arg Lys Arg Thr Ala His Glu Arg Gly Ala Arg Leu Val
7840 385             390             395             400
7843 Ala Ser Gly Glu Trp Ser Ser Gly Lys Arg Trp Ala Asp Asp Ala Pro
7844             405             410             415
7847 Gln Glu His Leu Asp Ala Gln Ser Ile Ser Ile Ile Ala Ser Gly Ala
7848             420             425             430
7851 Cys Gly Ala Leu Ile His Gly Leu Glu Asp Glu Phe Leu Glu Val Arg
7852         435             440             445
7855 Thr Ala Ala Val Ala Ser Met Cys Lys Leu Ala Leu Ser Arg Pro Asp
7856     450             455             460
7859 Phe Ala Val Thr Ser Leu Asp Phe Leu Val Asp Met Phe Asn Asp Glu
7860 465             470             475             480
7863 Ile Glu Asp Val Arg Leu Lys Ala Ile Tyr Ser Leu Thr Ala Ile Ala
7864             485             490             495
7867 Lys His Ile Val Leu Arg Glu Asp Gln Leu Glu Ile Met Leu Gly Ser
7868             500             505             510
7871 Leu Glu Asp Tyr Ser Val Asp Val Arg Glu Gly Leu His Leu Met Leu
7872         515             520             525
7875 Gly Ala Cys Arg Val Ser Thr Gln Thr Cys Leu Leu Met Val Val Gln
7876     530             535             540
7879 Lys Leu Leu Asp Val Leu Ala Lys Tyr Pro Gln Asp Arg Asn Ser Thr
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RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: US/10/527,571   TIME: 15:59:57

Input Set : **N:\SMITH\PTO.TS.txt**
Output Set: **N:\CRF4\01312006\J527571.raw**

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7880 545                   550                  555                  560
7883 Tyr Ala Cys Met Arg Lys Ile Gly Gln Lys His Pro His Leu Val Met
7884                   565                  570                  575
7887 Ala Val Ala Val His Leu Leu Tyr Val His Pro Phe Phe Glu Thr Pro
7888                   580                  585                  590
7891 Glu Arg Asp Val Glu Asp Pro Ala Tyr Leu Cys Val Leu Ile Leu Val
7892             595                  600                  605
7895 Phe Asn Ala Ala Glu His Leu Val Pro Ile Ile Ser Leu Leu Pro Thr
7896       610                  615                  620
7899 Ala Thr His Arg His Tyr Ala Tyr Leu Arg Asp Ser Met Pro Asn Leu
7900 625                   630                  635                  640
7903 Val Pro Gln Leu Pro Ile Glu Gly Ala Ser Ser Ala Ser Ala Thr His
7904                   645                  650                  655
7907 Arg Ile Asp Ser Ala Met His Gln Ala Gly Ser Ser Ala Glu Tyr Leu
7908             660                  665                  670
7911 Gln Met Ile Leu Ser His Ile Glu Glu Ile Phe Thr Met Thr Asp Glu
7912       675                  680                  685
7915 Arg Leu Glu Leu Leu Gln Thr Ala Gln Ser Asn Leu Gln Arg Leu Gly
7916       690                  695                  700
7919 Ser Ile Asp Ala Gly Met Tyr Gly Thr Ser Asn Phe Leu Glu Thr Phe
7920 705                   710                  715                  720
7923 Leu Ala Ala Gln Ile Gln Ile Glu Gln Met Gln Arg Cys Ala Ser Thr
7924             725                  730                  735
7927 Gln Arg Ser Arg Val Pro Leu Lys Glu Ser Leu Ala Ala Leu Ile Arg
7928             740                  745                  750
7931 Asn Cys Leu Lys Leu Gln His Thr Phe Ser Gly Leu Asn Tyr Gly Asp
7932       755                  760                  765
7935 Ile Leu Gln Val Lys Gln Leu Arg Leu Arg Ala Cys Ala Leu His Leu
7936       770                  775                  780
7939 Val Leu Val Val Arg Asp Arg Ser Gln Ser Ala Leu Gly Pro Cys Gln
7940 785                   790                  795                  800
7943 Met Leu Leu Gln Thr Ala Gly Asp Ile Ser Glu Phe Ile Lys Ala Asn
7944             805                  810                  815
7947 Thr Lys Asp Glu Glu Glu Lys Pro Pro Val Val Glu Thr Asp Met Pro
7948             820                  825                  830
7951 Met Lys Glu Ser Val Ser Arg Asp Ala Gln Pro Asp Ser Phe Thr Arg
7952       835                  840                  845
7955 Gln Leu Leu Ile Lys Leu Asp Gly Ile Ser Asp Pro Lys Pro Gly Arg
7956       850                  855                  860
7959 Val Phe Arg Glu Ile Leu Pro Leu Val Gln Gln Ala Pro Pro Leu Ala
7960 865                   870                  875                  880
7963 Leu Pro Pro Ala Asn Asp Lys Ile Arg Arg Cys Val Ala Asn Ile Leu
7964             885                  890                  895
7967 Glu Pro Cys Pro Leu Gln Ser Gln Asp Asn Val Ile Lys Val Thr Ala
7968             900                  905                  910
7971 Gly Leu Ile Ala Ala Val Pro Phe Val Ala Glu Ile Asp Asn Leu Leu
7972       915                  920                  925
7975 Glu Ser Gln Lys Ala Asp Met Arg Ile Lys Ile Lys Tyr Pro Asp Gln
7976       930                  935                  940
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RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: **US/10/527,571**   TIME: 15:59:57

Input Set : **N:\SMITH\PTO.TS.txt**
Output Set: **N:\CRF4\01312006\J527571.raw**

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      7979 His Met His Thr Val Val Pro Lys Gln Ser Asp Phe Lys Pro Ile Met
      7980 945                 950                 955                 960
      7983 Thr Glu Gln Gly Glu His Lys Thr Asn Val Arg Leu Arg Thr Thr Ile
      7984                 965                 970                 975
      7987 Leu Leu Ser His Ser Val Trp Thr Glu Ser Ser Leu Val Glu Ile Gln
      7988                 980                 985                 990
      7991 Leu Cys Leu Ala Val Arg Pro Gly  Ser Glu Leu Glu Leu  Cys Lys Pro
      7992             995                 1000                1005
      7995 Ala Lys  Val Leu Phe Ala Pro  Lys Pro Val Arg Arg  Gly Ile
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      8001 <212> TYPE: DNA
      8002 <213> ORGANISM: Drosophila melanogaster
      8004 <220> FEATURE:
      8005 <221> NAME/KEY: CDS
      8006 <222> LOCATION: (1)..(780)
      8007 <223> OTHER INFORMATION: CT7760
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      8012 Met Thr Thr Ala Ala Arg Pro Thr Phe Asp Pro Ala Arg Gly Gly Ser
      8013 1               5                   10                  15
      8015 ggt cgc ggc gaa aag gat ctg agt gca ctg agc aag cag tac tcc agt      96
      8016 Gly Arg Gly Glu Lys Asp Leu Ser Ala Leu Ser Lys Gln Tyr Ser Ser
      8017             20                  25                  30
      8019 cgc gat ttg cca ggc cac acg aaa ctg aaa tac agg gag act ggc cag     144
      8020 Arg Asp Leu Pro Gly His Thr Lys Leu Lys Tyr Arg Glu Thr Gly Gln
      8021             35                  40                  45
      8023 ggc acc agc gat gag aac cgc aac cgt gac ttc cgc aag gag ctg gag     192
      8024 Gly Thr Ser Asp Glu Asn Arg Asn Arg Asp Phe Arg Lys Glu Leu Glu
      8025         50                  55                  60
      8027 gag cgc gaa cgt gag gcg cgc tcc gga acg gga gcc act tcg tcg tcg     240
      8028 Glu Arg Glu Arg Glu Ala Arg Ser Gly Thr Gly Ala Thr Ser Ser Ser
      8029 65                  70                  75                  80
      8031 tcg ggc aag gca ctg ccc tcc att gta cgc aag gcg att gag gcg aac     288
      8032 Ser Gly Lys Ala Leu Pro Ser Ile Val Arg Lys Ala Ile Glu Ala Asn
      8033             85                  90                  95
      8035 aac gcc ggc ggt ggc agc agt gcc gca aag cgt tcc aag ccg gac gca     336
      8036 Asn Ala Gly Gly Gly Ser Ser Ala Ala Lys Arg Ser Lys Pro Asp Ala
      8037             100                 105                 110
      8039 ggg cag cag caa gcg cag cag gcg gct cag cag cag gcc gcc aat atg     384
      8040 Gly Gln Gln Gln Ala Gln Gln Ala Ala Gln Gln Gln Ala Ala Asn Met
      8041             115                 120                 125
E-->  8043 gac gcc gat gag ccg ctg gac aac gat agc tcc gac agc gat           432
      8044 Asp Ala Asp Glu Pro Leu Asp Asn Asp Ser Ser Asp Ser Asp
      8045     130                 135                 140
E-->  8047 tcc gat gac gat gat gcc gcc ctg ctg gcc gag ctg cag aag atc aag     480
      8048 Ser Asp Asp Asp Asp Ala Ala Leu Leu Ala Glu Leu Gln Lys Ile Lys
      8049 145                 150                 155                 160
```

```
E--> 8051 cag gaa cgt ctg cag gag acg gcg cgt cgc gag tcg gaa aag aag cag      528  522
     8052 Gln Glu Arg Leu Gln Glu Thr Ala Arg Arg Glu Ser Glu Lys Lys Gln
     8053             165                 170                 175
E--> 8055 gag gac gaa cgc ata cgc atg gag aac atc ctg tcc ggc aat cca ctg      576  570
     8056 Glu Asp Glu Arg Ile Arg Met Glu Asn Ile Leu Ser Gly Asn Pro Leu
     8057             180                 185                 190
E--> 8059 atg aac tat gag ccc ggc acc gcc gcc tcg gca gcg gga cgt gcc tct      624  618
     8060 Met Asn Tyr Glu Pro Gly Thr Ala Ala Ser Ala Ala Gly Arg Ala Ser
     8061             195                 200                 205
E--> 8063 gga ctg ggc ggt gat cta aag ata aag cgc cgc tgg gac gat gat gtg      672  666
     8064 Gly Leu Gly Gly Asp Leu Lys Ile Lys Arg Arg Trp Asp Asp Asp Val
     8065             210                 215                 220
E--> 8067 gtc ttt aag aat tgc gcc aga tct gcg ccc gat aag aag acg cac ttc      720  714
     8068 Val Phe Lys Asn Cys Ala Arg Ser Ala Pro Asp Lys Lys Thr His Phe
     8069 225                 230                 235                 240
E--> 8071 gtc aat gac gcc ctg cgc tcc gat ttc cac aag aag ttc atg gac aag      768  762
     8072 Val Asn Asp Ala Leu Arg Ser Asp Phe His Lys Lys Phe Met Asp Lys
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E--> 8075 tac att aag taa                                                      780  774
E--> 8076 Tyr Ile Lys
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     50814 <211> LENGTH: 522
     50815 <212> TYPE: PRT
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     50821 1               5                   10                  15
     50824 Asp Leu Val Arg Gln Leu Lys Ala Ala Lys Glu Ser Lys Glu Lys Ile
     50825             20                  25                  30
     50828 Asp Glu Glu Val Ala Arg Leu Leu Ala Leu Lys Ala Thr Leu Gly Gly
     50829             35                  40                  45
     50832 Asp Ala Ala Pro Thr Asn Gln Lys Phe Thr Leu Lys Thr Pro Lys Gly
     50833         50                  55                  60
     50836 Thr Arg Asp Tyr Gly Pro Gln Gln Met Thr Leu Arg Gln Gly Val Leu
     50837 65                  70                  75                  80
     50840 Asp Lys Ile Val Gln Val Phe Lys Arg His Gly Gly Glu Ala Ile Asp
     50841             85                  90                  95
     50844 Thr Pro Val Phe Glu Leu Lys Glu Val Leu Thr Gly Lys Tyr Gly Glu
     50845             100                 105                 110
     50848 Asp Ser Lys Leu Ile Tyr Asp Leu Lys Asp Gln Gly Gly Glu Ile Leu
     50849         115                 120                 125
     50852 Ser Met Arg Tyr Asp Leu Thr Val Pro Leu Ala Arg Tyr Leu Ala Met
     50853         130                 135                 140
     50856 Asn Lys Ile Ser Ser Ile Lys Arg Tyr His Ile Ala Lys Val Tyr Arg
     50857 145                 150                 155                 160
     50860 Arg Asp Asn Pro Ala Met Thr Lys Gly Arg Tyr Arg Glu Phe Tyr Gln
     50861             165                 170                 175
     50864 Cys Asp Phe Asp Ile Ala Gly Thr Tyr Asp Pro Met Leu Pro Asp Ala
     50865             180                 185                 190
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```
50868 Glu Cys Val Lys Ile Val Ser Glu Ile Leu Asp Thr Leu Asp Ile Gly
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50872 Asp Tyr Val Ile Lys Leu Asn His Arg Gln Leu Leu Asp Gly Met Phe
50873         210             215             220
50876 Gln Ala Cys Gly Val Pro Ala Asp Ser Phe Arg Thr Ile Cys Ser Ala
50877 225             230             235             240
50880 Val Asp Lys Leu Asp Lys Ser Pro Trp Ala Asp Val Arg Lys Glu Met
50881         245             250             255
50884 Val Asp Glu Lys Gly Leu Asp Glu Ala Ala Ala Asp Arg Ile Gly Glu
50885         260             265             270
50888 Tyr Val Arg Leu Ser Gly Gly Ala Glu Leu Val Glu Gln Leu Leu Ala
50889         275             280             285
50892 Asn Glu Lys Leu Lys Ala Val Pro Asn Ala Val Lys Gly Leu Glu Gly
50893         290             295             300
50896 Met Lys Gln Leu Leu Lys Tyr Cys Ser Ile Phe Gly Leu Asp Lys Arg
50897 305             310             315             320
50900 Val Ser Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly
50901         325             330             335
50904 Val Ile Tyr Glu Gly Val Leu Lys Gly Glu Ser Ala Thr Val Ala Ser
50905         340             345             350
50908 Pro Ala Lys Thr Ser Gln Gln Asn Gly Glu Gln Ala Asn Glu Pro Ala
50909         355             360             365
50912 Thr Val Gly Ser Val Ala Gly Gly Gly Arg Tyr Asp Asn Leu Val Gly
50913         370             375             380
50916 Met Phe Asp Pro Arg Gly Lys Ala Val Pro Cys Val Gly Val Ser Ile
50917 385             390             395             400
50920 Gly Val Glu Arg Ile Phe Ser Val Leu Glu Ala Arg Ala Ala Ala Ser
50921         405             410             415
50924 Gly Leu Lys Leu Arg Thr Ser Asp Val Glu Val Tyr Val Ala Ser Ala
50925         420             425             430
50928 His Lys Gly Leu His Glu Gln Arg Leu Lys Val Leu Asn Leu Leu Trp
50929         435             440             445
50932 Asp Ala Gly Val Lys Ala Glu His Ser Tyr Lys Leu Asn Pro Lys Leu
50933         450             455             460
50936 Leu Val Gln Leu Gln His Cys Glu Glu His Gln Ile Pro Leu Val Val
50937 465             470             475             480
50940 Val Leu Gly Asp Ala Glu Leu Ala Gln Gly Leu Val Lys Leu Arg Glu
50941         485             490             495
50944 Val Thr Thr Arg Glu Glu Thr Asn Val Lys Leu Glu Asp Leu Ala Ala
50945         500             505             510
50948 CT19850 Glu Ile Arg Arg Arg Gln Gln Ala Ser Ala
50949          515             520
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515   520

Pls delete

VERIFICATION SUMMARY   DATE: 01/31/2006
PATENT APPLICATION: **US/10/527,571**   TIME: 16:00:01

Input Set : **N:\SMITH\PTO.TS.txt**
Output Set: **N:\CRF4\01312006\J527571.raw**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:191 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:6917 M:280 W: Numeric Identifier already exists, Length not replaced.
L:7023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:1248.
L:7195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:400
L:7996 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61
L:8043 M:254 E: No. of Bases conflict, LENGTH:Input:432 Counted:426 SEQ:62
M:254 Repeated in SeqNo=62
L:8076 M:252 E: No. of Seq. differs, <211> LENGTH:Input:780 Found:774 SEQ:62
L:27070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:180 after pos.:1680
M:341 Repeated in SeqNo=180
L:27247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:181 after pos.:544
M:341 Repeated in SeqNo=181
L:33756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:204 after pos.:2976
M:341 Repeated in SeqNo=204
L:34026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:992
L:50948 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:50948 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:50949 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:299
L:50963 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:300,Line#:50960
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